

SEQUENCE LISTING

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<120> THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A Fc
EPSILON RECEPTOR ALPHA CHAIN AND A Fc REGION OF AN IgE
ANTIBODY AND USES THEREOF

<130> AL-8

<140> not yet assigned

<141> 2001-03-14

<150> 60/189,853

<151> 2000-03-15

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 528

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(528)

<400> 1

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Val	Pro	Gln	Lys	Pro	Lys	Val	Ser	Leu	Asn	Pro	Pro	Trp	Asn	Arg	Ile	
1				5					10					15		

ttt	aaa	gga	gag	aat	gtg	act	ctt	aca	tgt	aat	ggg	aac	aat	ttc	ttt	96
Phe	Lys	Gly	Glu	Asn	Val	Thr	Leu	Thr	Cys	Asn	Gly	Asn	Asn	Phe	Phe	
			20					25					30			

gaa	gtc	agt	tcc	acc	aaa	tgg	ttc	cac	aat	ggc	agc	ctt	tca	gaa	gag	144
Glu	Val	Ser	Ser	Thr	Lys	Trp	Phe	His	Asn	Gly	Ser	Leu	Ser	Glu	Glu	
			35				40					45				

aca	aat	tca	agt	ttg	aat	att	gtg	aat	gcc	aaa	ttt	gaa	gac	agt	gga	192
Thr	Asn	Ser	Ser	Leu	Asn	Ile	Val	Asn	Ala	Lys	Phe	Glu	Asp	Ser	Gly	
	50					55					60					

gaa tac aaa tgt cag cac caa caa gtt aat gag agt gaa cct gtg tac 240
 Glu Tyr Lys Cys Gln His Gln Gln Val Asn Glu Ser Glu Pro Val Tyr
 65 70 75 80

ctg gaa gtc ttc agt gac tgg ctg ctc ctt cag gcc tct gct gag gtg 288
 Leu Glu Val Phe Ser Asp Trp Leu Leu Leu Gln Ala Ser Ala Glu Val
 85 90 95

gtg atg gag ggc cag ccc ctc ttc ctc agg tgc cat ggt tgg agg aac 336
 Val Met Glu Gly Gln Pro Leu Phe Leu Arg Cys His Gly Trp Arg Asn
 100 105 110

tgg gat gtg tac aag gtg atc tat tat aag gat ggt gaa gct ctc aag 384
 Trp Asp Val Tyr Lys Val Ile Tyr Tyr Lys Asp Gly Glu Ala Leu Lys
 115 120 125

tac tgg tat gag aac cac aac atc tcc att aca aat gcc aca gtt gaa 432
 Tyr Trp Tyr Glu Asn His Asn Ile Ser Ile Thr Asn Ala Thr Val Glu
 130 135 140

gac agt gga acc tac tac tgt acg ggc aaa gtg tgg cag ctg gac tat 480
 Asp Ser Gly Thr Tyr Tyr Cys Thr Gly Lys Val Trp Gln Leu Asp Tyr
 145 150 155 160

gag tct gag ccc ctc aac att act gta ata aaa gct ccg cgt gag aag 528
 Glu Ser Glu Pro Leu Asn Ile Thr Val Ile Lys Ala Pro Arg Glu Lys
 165 170 175

<210> 2

<211> 176

<212> PRT

<213> Homo sapiens

<400> 2

Val Pro Gln Lys Pro Lys Val Ser Leu Asn Pro Pro Trp Asn Arg Ile
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Phe Lys Gly Glu Asn Val Thr Leu Thr Cys Asn Gly Asn Asn Phe Phe
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Glu Val Ser Ser Thr Lys Trp Phe His Asn Gly Ser Leu Ser Glu Glu
 35 40 45

Thr Asn Ser Ser Leu Asn Ile Val Asn Ala Lys Phe Glu Asp Ser Gly
 50 55 60

Glu Tyr Lys Cys Gln His Gln Gln Val Asn Glu Ser Glu Pro Val Tyr
 65 70 75 80

Leu Glu Val Phe Ser Asp Trp Leu Leu Leu Gln Ala Ser Ala Glu Val
 85 90 95

Val Met Glu Gly Gln Pro Leu Phe Leu Arg Cys His Gly Trp Arg Asn
 100 105 110

Trp Asp Val Tyr Lys Val Ile Tyr Tyr Lys Asp Gly Glu Ala Leu Lys
 115 120 125

Tyr Trp Tyr Glu Asn His Asn Ile Ser Ile Thr Asn Ala Thr Val Glu
 130 135 140

Asp Ser Gly Thr Tyr Tyr Cys Thr Gly Lys Val Trp Gln Leu Asp Tyr
 145 150 155 160

Glu Ser Glu Pro Leu Asn Ile Thr Val Ile Lys Ala Pro Arg Glu Lys
 165 170 175

<210> 3

<211> 528

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(528)

<400> 3

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 Val Pro Gln Lys Pro Lys Val Ser Leu Asn Pro Pro Trp Asn Arg Ile
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ttt aaa gga gag aat gtg act ctt aca tgt aat ggg aac aat ttc ttt 96
 Phe Lys Gly Glu Asn Val Thr Leu Thr Cys Asn Gly Asn Asn Phe Phe
 20 25 30

gaa gtc agt tcc acc aaa tgg ttc cac aat ggc agc ctt tca gaa gag 144
 Glu Val Ser Ser Thr Lys Trp Phe His Asn Gly Ser Leu Ser Glu Glu
 35 40 45

aca aat tca agt ttg aat att gtg aat gcc aaa ttt gaa gac agt gga 192
 Thr Asn Ser Ser Leu Asn Ile Val Asn Ala Lys Phe Glu Asp Ser Gly
 50 55 60

gaa tac aaa tgt cag cac caa caa gtt gct gag agt gaa cct gtg tac 240
 Glu Tyr Lys Cys Gln His Gln Gln Val Ala Glu Ser Glu Pro Val Tyr
 65 70 75 80

ctg gaa gtc ttc agt gac tgg ctg ctc ctt cag gcc tct gct gag gtg 288
 Leu Glu Val Phe Ser Asp Trp Leu Leu Leu Gln Ala Ser Ala Glu Val
 85 90 95

gtg atg gag ggc cag ccc ctc ttc ctc agg tgc cat ggt tgg agg aac 336
 Val Met Glu Gly Gln Pro Leu Phe Leu Arg Cys His Gly Trp Arg Asn
 100 105 110

tgg gat gtg tac aag gtg atc tat tat aag gat ggt gaa gct ctc aag 384
 Trp Asp Val Tyr Lys Val Ile Tyr Tyr Lys Asp Gly Glu Ala Leu Lys
 115 120 125

tat tgg tat gag aac cac gct atc tcc att aca aat gcc gca gct gaa 432
 Tyr Trp Tyr Glu Asn His Ala Ile Ser Ile Thr Asn Ala Ala Glu
 130 135 140

gac agt gga acc tac tac tgt acg ggc aaa gtg tgg cag ctg gac tat 480
 Asp Ser Gly Thr Tyr Tyr Cys Thr Gly Lys Val Trp Gln Leu Asp Tyr
 145 150 155 160

gag tct gag ccc ctc aac att act gta ata aaa gct ccg cgt gag aag 528
 Glu Ser Glu Pro Leu Asn Ile Thr Val Ile Lys Ala Pro Arg Glu Lys
 165 170 175

<210> 4

<211> 176

<212> PRT

<213> Homo sapiens

<400> 4

Val Pro Gln Lys Pro Lys Val Ser Leu Asn Pro Pro Trp Asn Arg Ile
 1 5 10 15

Phe Lys Gly Glu Asn Val Thr Leu Thr Cys Asn Gly Asn Asn Phe Phe
 20 25 30

Glu Val Ser Ser Thr Lys Trp Phe His Asn Gly Ser Leu Ser Glu Glu
 35 40 45

Thr Asn Ser Ser Leu Asn Ile Val Asn Ala Lys Phe Glu Asp Ser Gly
 50 55 60

Glu Tyr Lys Cys Gln His Gln Gln Val Ala Glu Ser Glu Pro Val Tyr
65 70 75 80

Leu Glu Val Phe Ser Asp Trp Leu Leu Leu Gln Ala Ser Ala Glu Val
85 90 95

Val Met Glu Gly Gln Pro Leu Phe Leu Arg Cys His Gly Trp Arg Asn
100 105 110

Trp Asp Val Tyr Lys Val Ile Tyr Tyr Lys Asp Gly Glu Ala Leu Lys
115 120 125

Tyr Trp Tyr Glu Asn His Ala Ile Ser Ile Thr Asn Ala Ala Ala Glu
130 135 140

Asp Ser Gly Thr Tyr Tyr Cys Thr Gly Lys Val Trp Gln Leu Asp Tyr
145 150 155 160

Glu Ser Glu Pro Leu Asn Ile Thr Val Ile Lys Ala Pro Arg Glu Lys
165 170 175

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<211> 669

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(666)

<400> 5

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cgg ccc agc ccg ttc gac ctg ttc atc cgc aag tcg ccc acg atc acc 96
Arg Pro Ser Pro Phe Asp Leu Phe Ile Arg Lys Ser Pro Thr Ile Thr
20 25 30

tgt ctg gtg gtg gac ctg gca ccc agc aag ggg acc gtg aac ctg acc 144
Cys Leu Val Val Asp Leu Ala Pro Ser Lys Gly Thr Val Asn Leu Thr
35 40 45

tgg tcc cgg gcc agt ggg aag cct gtg aac cac tcc acc aga aag gag 192
Trp Ser Arg Ala Ser Gly Lys Pro Val Asn His Ser Thr Arg Lys Glu
50 55 60

gag aag cag cgc aat ggc acg tta acc gtc acg tcc acc ctg ccg gtg 240
 Glu Lys Gln Arg Asn Gly Thr Leu Thr Val Thr Ser Thr Leu Pro Val
 65 70 75 80

ggc acc cga gac tgg atc gag ggg gag acc tac cag tgc agg gtg acc 288
 Gly Thr Arg Asp Trp Ile Glu Gly Glu Thr Tyr Gln Cys Arg Val Thr
 85 90 95

cac ccc cac ctg ccc agg gcc ctc atg cgg tcc acg acc aag acc agc 336
 His Pro His Leu Pro Arg Ala Leu Met Arg Ser Thr Thr Lys Thr Ser
 100 105 110

ggc ccg cgt gct gcc ccg gaa gtc tat gcg ttt gcg acg ccg gag tgg 384
 Gly Pro Arg Ala Ala Pro Glu Val Tyr Ala Phe Ala Thr Pro Glu Trp
 115 120 125

ccg ggg agc cgg gac aag cgc acc ctc gcc tgc ctg atc cag aac ttc 432
 Pro Gly Ser Arg Asp Lys Arg Thr Leu Ala Cys Leu Ile Gln Asn Phe
 130 135 140

atg cct gag gac atc tcg gtg cag tgg ctg cac aac gag gtg cag ctc 480
 Met Pro Glu Asp Ile Ser Val Gln Trp Leu His Asn Glu Val Gln Leu
 145 150 155 160

ccg gac gcc cgg cac agc acg acg cag ccc cgc aag acc aag ggc tcc 528
 Pro Asp Ala Arg His Ser Thr Thr Gln Pro Arg Lys Thr Lys Gly Ser
 165 170 175

ggc ttc ttc gtc ttc agc cgc ctg gag gtg acc agg gcc gaa tgg gag 576
 Gly Phe Phe Val Phe Ser Arg Leu Glu Val Thr Arg Ala Glu Trp Glu
 180 185 190

cag aaa gat gag ttc atc tgc cgt gca gtc cat gag gca gcg agc ccc 624
 Gln Lys Asp Glu Phe Ile Cys Arg Ala Val His Glu Ala Ala Ser Pro
 195 200 205

tca cag acc gtc cag cga gcg gtg tct gta aat ccc ggt aaa tga 669
 Ser Gln Thr Val Gln Arg Ala Val Ser Val Asn Pro Gly Lys
 210 215 220

<210> 6
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 <213> Homo sapiens

<400> 6

Ala Asp Pro Cys Asp Ser Asn Pro Arg Gly Val Ser Ala Tyr Leu Ser
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 20 25 30

Cys Leu Val Val Asp Leu Ala Pro Ser Lys Gly Thr Val Asn Leu Thr
 35 40 45

Trp Ser Arg Ala Ser Gly Lys Pro Val Asn His Ser Thr Arg Lys Glu
 50 55 60

Glu Lys Gln Arg Asn Gly Thr Leu Thr Val Thr Ser Thr Leu Pro Val
 65 70 75 80

Gly Thr Arg Asp Trp Ile Glu Gly Glu Thr Tyr Gln Cys Arg Val Thr
 85 90 95

His Pro His Leu Pro Arg Ala Leu Met Arg Ser Thr Thr Lys Thr Ser
 100 105 110

Gly Pro Arg Ala Ala Pro Glu Val Tyr Ala Phe Ala Thr Pro Glu Trp
 115 120 125

Pro Gly Ser Arg Asp Lys Arg Thr Leu Ala Cys Leu Ile Gln Asn Phe
 130 135 140

Met Pro Glu Asp Ile Ser Val Gln Trp Leu His Asn Glu Val Gln Leu
 145 150 155 160

Pro Asp Ala Arg His Ser Thr Thr Gln Pro Arg Lys Thr Lys Gly Ser
 165 170 175

Gly Phe Phe Val Phe Ser Arg Leu Glu Val Thr Arg Ala Glu Trp Glu
 180 185 190

Gln Lys Asp Glu Phe Ile Cys Arg Ala Val His Glu Ala Ala Ser Pro
 195 200 205

Ser Gln Thr Val Gln Arg Ala Val Ser Val Asn Pro Gly Lys
 210 215 220